Amendments to the Claims:

This listing of claims replaces all prior versions and listings of claims in the application:

Listing of Claims:

1-12. Canceled

13. (New): A method for determining the presence or absence of a single nucleotide polymorphism (SNP) in an OATP-C gene, the method comprising

(a) providing a nucleic acid sample from a human identified as in need of treatment with a therapeutic agent that is transported by OATP-C, wherein the sample comprises a nucleotide at a position corresponding to position 1561 of SEQ ID NO: 1, and

(b) testing the sample to determine the identity of the nucleotide.

14. (New): The method of claim 13, wherein the nucleic acid sample comprises a fragment of an OATP-C DNA.

15. (New): The method of claim 13, wherein the human is in need of treatment with a statin.

16. (New): The method of claim 13, wherein the human is in need of treatment with a xenobiotic.

17. (New): The method of claim 13, wherein step (b) comprises performing a method selected from the group consisting of an ARMS™ or ALEX™ assay, COPS, Taqman™, Molecular Beacons, RFLP, restriction site based PCR and FRET.

18. (New): The method of claim 13, wherein the nucleotide is a C.

19. (New): The method of claim 13, wherein the nucleotide is not a G.

20. (New): The method of claim 13, wherein the nucleotide is in a codon that does not encode a glycine.

21. (New): The method of claim 13, wherein the nucleotide is in a codon that encodes an arginine.

22. (New): A method for determining the presence or absence of a single nucleotide polymorphism (SNP) in an OATP-C gene, the method comprising:

(a) providing a nucleic acid sample from a human having or at risk for developing an OATP-C-mediated disease, wherein the sample comprises a nucleotide at a position corresponding to position 1561 of SEQ ID NO: 1; and

(b) testing the sample to determine the identity of the nucleotide.

23. (New): The method of claim 22, wherein the human has or is at risk for developing hyperlipoproteinemia.

24. (New): The method of claim 22, wherein the human has or is at risk for developing cardiovascular disease.

25. (New): A method for determining the presence or absence of a SNP in an OATP-C gene, the method comprising

(a) providing a nucleic acid sample from a human, wherein the sample comprises a nucleotide at a position corresponding to position 1561 of SEQ ID NO: 1; and

(b) determining the identity of the nucleotide by using a method selected from the group consisting of an ARMS™ or ALEX™ assay, COPS, Taqman™, Molecular Beacons, RFLP, restriction site based PCR and FRET.

26. (New): A method for determining the presence or absence of a SNP in an OATP-C gene of a human, the method comprising

(a) providing a fragment of an OATP-C nucleic acid from the human, wherein the fragment comprises a nucleotide at a position corresponding to position 1561 of SEQ ID NO:1; and

(b) determining the identity of the nucleotide by using a method selected from the group consisting of an ARMS™ or ALEX™ assay, COPS, Taqman™, Molecular Beacons, RFLP, restriction site based PCR and FRET.

27. (New): A method for identifying the presence of a SNP in an OATP-C gene in a nucleic acid sample of a human, the method comprising determining that the nucleotide in the sample corresponding to position 1561 of SEQ ID NO: 1 is a C.

28. (New): A method for identifying the presence of a SNP in an OATP-C gene in a nucleic acid sample of a human, the method comprising determining that the nucleotide in the sample corresponding to position 1561 of SEQ ID NO: 1 is not a G.

29. (New): A method for identifying the presence of a SNP in an OATP-C gene in a nucleic acid sample of a human, the method comprising determining that the nucleotide in the sample corresponding to position 1561 of SEQ ID NO: 1 is in a codon that does not encode a glycine.

30. (New): A method for identifying the presence of a SNP in an OATP-C gene in a nucleic acid sample of a human, the method comprising determining that the nucleotide in the sample corresponding to position 1561 of SEQ ID NO: 1 is in a codon that encodes an arginine.

31. (New): A method to assess the pharmacogenetics of a drug, the method comprising

(a) providing a nucleic acid sample from a human, wherein the sample comprises a nucleotide at a position corresponding to position 1561 of SEQ ID NO: 1;

(b) determining the identity of the nucleotide; and

(c) correlating (i) the identity of the nucleotide to (ii) the human's response following administration of the drug, thereby assessing the pharmacogenetics of the drug.

32. (New): A method for determining the presence or absence of at least one SNP in an OATP-C gene, the method comprising

(a) providing a nucleic acid sample from a human, wherein the sample comprises nucleotides at positions corresponding to

positions 510, 696, 1299, 1312, 1347, 1561, 2028, 2327, and 2342 of SEQ ID NO:1,

positions 321 and 1332 of SEQ ID NO:3,

position 41 of SEQ ID NO:4,

positions 109 and 244 of SEQ ID NO:5,

positions 117 and 283 of SEQ ID NO:6,

positions 209 and 211 of SEQ ID NO:7,

positions 63 through 68 of SEQ ID NO:8,

position 53 of SEQ ID NO:9,

position 75 of SEQ ID NO:10,

position 162 of SEQ ID NO:11, and

position 84 of SEQ ID NO:12; and

(b) determining the identity of at least one of the nucleotides by a method selected from the group consisting of an ARMS™ or ALEX™ assay, COPS, Taqman™, Molecular Beacons, RFLP, restriction site based PCR and FRET.

33. (New): The method of claim 32, wherein the identities of all 28 of the nucleotides are determined.

34. (New): A method of treatment comprising:

(a) identifying a patient in need of treatment with a therapeutic agent that is transported by OATP-C;

(b) determining whether the patient has a glycine at the amino acid position of OATP-C corresponding to position 488 of SEQ ID NO:2; and

(c) prescribing an appropriate dosage of the therapeutic agent.

35. (New): A method of treatment comprising:

(a) identifying a patient having or at risk for developing an OATP-C-mediated disease;

(b) determining whether the patient has a glycine at the amino acid position of OATP-C corresponding to position 488 of SEQ ID NO:2; and

(c) prescribing an appropriate dosage of the therapeutic agent.

36. (New): The method of claim 35, wherein step (b) comprises:

(i) providing a nucleic acid sample from the patient, wherein the sample comprises a nucleotide at a position corresponding to position 1561 of SEQ ID NO: 1; and

(ii) determining the identity of the nucleotide by use of a method selected from the group consisting of an ARMS™ or ALEX™ assay, COPS, Taqman™, Molecular Beacons, RFLP, restriction site based PCR and FRET.

37. (New): The method of claim 35 comprising determining that the patient does not have a glycine at the amino acid position of OATP-C corresponding to position 488 of SEQ ID NO:2.

38. (New): The method of claim 35 comprising determining that the patient has an arginine at the amino acid position of OATP-C corresponding to position 488 of SEQ ID NO:2.

39. (New): An isolated nucleic acid encoding a protein comprising the amino acid sequence of SEQ ID NO:2, wherein the amino acid at the position corresponding to position 488 of SEQ ID NO:2 is not glycine.

40. (New): An isolated nucleic acid comprising SEQ ID NO:1, wherein the nucleotide of the nucleic acid at the position corresponding to position 1561 of SEQ ID NO:1 is a C.

41. (New): An isolated nucleic acid that hybridizes under stringent conditions with a probe consisting of the nucleotide sequence of SEQ ID NO:1 or the complement thereof, wherein the nucleotide of the probe at the position corresponding to position 1561 of SEQ ID NO:1 is a C.

42. (New): A polypeptide comprising the amino acid sequence of SEQ ID NO:2, wherein the amino acid corresponding to position 488 of SEQ ID NO:2 is not glycine.

43. (New): A polypeptide comprising a fragment of the amino acid sequence of SEQ ID NO:2 at least 10 amino acids in length, wherein the polypeptide comprises an amino acid corresponding to position 488 of SEQ ID NO:2 and that amino acid is not a glycine.

44. (New): An antibody that binds to human OATP-C when the amino acid corresponding to position 488 of SEQ ID NO:2 is arginine, but not when the amino acid at position 488 is glycine.

45. (New): A method of performing a linkage study, the method comprising

(a) providing a nucleic acid sample from each of two or more humans having or at risk for having an OATP-C-mediated disease, wherein the sample comprises a nucleotide at a position corresponding to position 1561 of SEQ ID NO:1;

(b) testing each sample to determine the identity of the nucleotide; and

(c) comparing (i) the frequency with which a C occurs at the position corresponding to position 1561 of SEQ ID NO:1 in the samples, with (ii) the frequency with which C occurs at the position corresponding to position 1561 of SEQ ID NO:1 in nucleic acid samples from the population at large.